

Figure 1

MKEIAMNNSKRKPEPPFAGKKLSTRRKRKAQISPLVQSPPLWSKQIGVSAASVDSQCS
60
DLIADDNVSCGSSRVKEKSNPKKTLIEVEVKPGYVNKETIGDSKPRRIITRSYSKLHKE
KEGDELEVSSESCVDSNSGAGLRIRNMYGNKINDNDEISFSRSDVTPAGHVSNSRSLNFE
120
SENKESDVSDFVSVISGVEVCSKFGSVTGGADNEELIEISKPSSFVEADSSIGSAKELKPELFI
240
VGCVDLACSEKFKSEEYSDLDSESSORSEIISQYSDDYSDYTPSITFDGSEFSEKS
300
SSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEELHSSELIRFDDEEVESYLRLRERE
360
RSHAYMRUCAKAYCSRDMDNTGLIPRURSIMVOWIVIQCSDMGLQOETLFLGVGLIDRPLS
420
KGSKFKSERTLLIVGTLASLTLATRIEENQYNNSIRKENFTIONLRYSRHEVVAMEMLYQEV
480
LNFKCFPTTIFNFWFYIKAARANPEVERKAKSILAVTSLSQTQLCFWPSTVAAAIVVLA
540
CIEHNKISAYQRVIVKVHVRRTIDNEIFPVCVKSLIDWLIQ
578

Figure 2

SDS	377	MDN-TGLIPRLRSIMQWIVKQCSDMGLQQETLFLGVGILLDRFLSKGSF	424
cyc2b		MAQQFDISDKMRALLIDWLIEVHDKFELMNETLFITVNLLIDRFLSKQAV	
cyc2a		M-QQDLINEKMRALLIDWLIEVHDKFDLMNETLFITVNLLIDRFLSKQNV	
Consensus	M	+ + +R+I++ W++	L +ETLFL+V L+DRFLSK
SDS	425	KSERTLILVGIASTLATRIEE-NOPYNSIRKRNFNTIONLRYSRHEVVA	472
cyc2b		-ARKKLQLVGLVALLLACKYEVSVP---IVEDLVVISDKAYTRNDVLE	
cyc2a		-MRKKLQLVGLVALLLACKYEVSVP---VVEDLVLIISDKAYTRNDVLE	
Consensus		+ L LVG+ +L LA + EE P + I	Y+R +V+
SDS	473	MEWLVQEVLNEFKCFTPTIFNFWFYLKAAARANPEVERKAKSLAVTSLSD	521
cyc2b		MEKIMLSTLQFNMSLPTQYPFLKREFLKAAQSDDKLETLIASFLIELALVD	
cyc2a		MEKIMLSTLQFNMSLPTQYPFLKREFLKAAQADKKCEVTLASFLIELALVE	
Consensus	ME	- L+F PT + FL +LKAA A E A L +L D	

Figure 3

	cyc2b	cyc2a	cyc3b	cycD
SDS	100%	34%/52%	34%/52%	28%/49%
		100%	87%/92%	40%/60%
cyc2b			100%	46%/64%
cyc2a				22%/43%
cyc3b			100%	22%/41%